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Fig. 1A

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Title: Stem Cell Maintenance Factor Materials and Methods Docket No. 28110/35905A Page 2 of 9 Fig. 1B

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ilG. 1B

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- I R E -	250 260 270 280	FDPRAKIEIREFKMELWPGYET	FNWGDSRAVPDYNMSILPGYBTAIR	YDPOAKINLENFRMQLWPGYQTSIRQHE		1 7 1 1 W 2	310	V MRTETIYDIMRRCSHNPARHQDEVRVNVLDL 1 V L 1	M V R E E S M Y I L F H K E L R S C O N N P O R V O E K M N E M Y G G	V MRTETLYNILSDAIRDSDDYQSTFKRAVMGMVILT	D Y N N K L H R I T D V D F - I T P L S K F - K D G - X I S L V E Y Y K N Q Y N Majority	1	DYNNRTYRINDVDFGQTPKSTFSCKGRDISFVEY	THE TERMS AND THE TERMS AND THE TERMS AND THE TERMS AND AND THE TERMS AND AND THE TERMS AND AND THE TERMS AND THE	RYNNKLHRITRLDNEITPLSKFOKDGEOILL	DYNNKTYRIDDVDFQSTPLCKFKTNDGEISYVDIXKNKLM	4	ETTDLKOPLLISEGKDKQ-PGGP-PQVAILLEDCKT	
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FIG. 10

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Fig. 1D

ELCRVTG piwi.PRO ELCYLTG hiwi.PRO ELCFPTG ciwi2.PRO ELCFPTG ciwi1.PRO ELARATG aubergine.PRO	A L I X R L S K N Majority 440 A F N H R L Q N T piwi.PRO K L I V D L S K N ciwi2.PRO K L I T K L S Q N ciwi1.PRO M F N K R L K S C aubergine.PRO	480 480 VEH-NGKVP piwi.PROHQGKTF hiwi.PROQ-GKTTY ciwi2.PROQ-GKTTY ciwi2.PROQ-GKTTY ciwi1.PROQ-GKTTY ciwi1.PROQ-GKTTY ciwi1.PRO
390 R D K A L K T N A - S E L V V L I P K P K Q - P G G T L P G P A M L I P K P K Q - P G E P - P Q V S Y I V P K P K Q - P G E P - P Q V S Y I V P T D K N I R G G N - D Q A I M I I P	8 L R K 430 R L R R R R R R R R R R R R R R R R R	ARVLKSEKI
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FIG. 11

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1G. 1E

Title: Stem Cell Maintenance Factor Materials and Methods Docket No. 28110/35905A Page 6 of 9 Fig. 1F

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FIG. 11

R T L P S R I I V Y R D G V G D G Q L K T L V N T E V K D A V T D L MAJORILY 730 740 750 740 750 760 761 8135 E Y M P S R I I V Y R D G V G G G L K T L V N T E V K L V R D A C D A V T D K CIMIL PRO 815 E Y M P S R I I V Y R D G V G D G Q L K T L V N T E V K L V R D A C D A V T D K CIMIL PRO 854 I K T L P E R I L L E P D G V G D G Q L K T L L R N T E V K L V R D A C D A V T D K CIMIL PRO 856 [R] E L P E R I L L E P R D G V G D G Q L K T L L R N T E V K L V R D A C D A V T D K CIMIL PRO 856 [R] E L P E R I L L E P R D G V G D G Q L K T L L E Y R V R V N T R F T Q G G L L S S V him L H Y PRO 857
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088	NVLYSSMGLSPEKMOKLTYKMCHLYYNWSGTTRVPAVCOY piwi.PRO 457 NVIYDNSGLKPDHIQRLTYKLCHIYYNWPGVIRVPAPCOY hiwi.PRO 758 NIIHDDTDLGPDKHQOLAFKLCHLYYNWQGTVRVPAPCOY ciwi2.PRO 656 NIIHDDTGLGPDKHQQLAFKLCHLYYNWQGTVRVPAPCOY 800 NVISDNMGLNADKLQMLSYKMTHMYYNYSGTIRVPAVCHY aubergine.PRO 186	Majority piwi.PRO hiwi.PRO ciwi2.PRO ciwi1.PRO aubergine.PRO hiwi_Hy.PRO	
870	IXXNWSGTTRVPIXYNWQGTVRVPLXXNWQGTVRVPMQGTVRVPMXXNXSGTIRVP	I Y F I I F F I I Y Y I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I I I F F I F F F F I F F F I F	decii tile collisellada tada
098	EKMOKLTYKLCH DHIORLTYKLCH DKHOQLAFKLCH DKHOQLAFKLCH	AHKLAFLVAQSLHDDPNGXLRDKLYFL 890 AKKLATLVGTNLHSIPQNALEKKEYYL AHKLAFLVGQSLHDDANGCLRDKLFFL AHKLAFLTAQSLHDDANGCLRDKLFFL AHKLAFLTAQSLHDDANGYLRDKLFFL AHKLAFLVAESINRAPSAGLQNQLYFL	I : DOY TESTAMES THAT IN
850	N V L Y S S M G L S P E K M Q K L T Y K M C H L Y Y N W S G T T R V P A V C Q Y PIWI.PRO 457 N V I Y D N S G L K P D H I Q R L T Y K L C H I Y Y N W P G V I R V P A P C Q Y PIWI.PRO 758 N I I H D D T D L G P D K H Q Q L A F K L C H L Y Y N W Q G T V R V P A P C Q Y CIWI2.PRO 656 N I I H D D T G L G P D K H Q Q L A F K L C H L Y Y N W Q G T V R V P A P C Q Y CIWI1.PRO 800 N V I S D N M G L N A D K L Q M L S Y K M T H M Y Y N Y S G T I R V P A V C H Y A Ubergine 186	818 A K L A F L V A Q S L H D D P N G X L R D K L Y F L 890 900 917 A H K L A T L V G T N L H S I P Q N A L E K K F Y Y L 798 A H K L A F L T A Q S L H D D A N G C L R D K L F F L 840 A H K L A F L T A Q S L H D D A N G Y L R D K L F F L 840 A H K L A F L V A E S I N R A P S A G L Q N Q L Y F L 840 A H K L A F L V A E S I N R A P S A G L Q N Q L Y F L	Decoration Decoration #

Decoration 'Decoration #2': Shade (with black at 10% fill) residues that match hiwi_Hy.PRO exactly.

FIC. II

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SEQUENCE ALIGNMENT

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MVV 60	KKY 120 KKY 326	2FF 18		
SIKKYLS <u>SD</u> CPVPSQCV <u>L</u> ARTLNKQGMMMSIATKIAMQMTCKLGGELWAVEIPLKSLMVV 60	GIDVCKDALSKDVMVVGCVASVNPRITRWFSRCILQRTMTDVADCLKVFMTGALNKWYKY 120 GIDVCKDALSKDVMVVGCVASVNPRITRWFSRCILQRTMTDVADCLKVFMTGALNKWYKY 326	NHDLPARIIVYRAGVGDGQLKTLIEYEVPQLLSSVAESSSNTSSRLSVIVVRKKCMPRFF 180 NHDLPARIIVYRAGVGDGQLKTLIEYEVPQLLSSVAESSSNTSSRLSVIVVRKKCMPRFF 386	TEMNRT 186 TEMNRT 392	= 942 (336.7 bits), Expect = 3.0e-100, P = 3.0e-100 ities = 183/186 (98%), Positives = 183/186 (98%)
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